In developing countries, maternal death is recognized as one of the major public health problems and occurs at a higher rate in postpartum period globally (nearly 40%) than in antepartum, intrapartum, and late periods. Sepsis (puerperal sepsis), which is one of the four major causes of maternal deaths worldwide, is common in developing countries. Particularly in South Asia, the estimated number and proportion of sepsis among causes of maternal deaths is the highest in the world. Puerperal sepsis is an infective condition in puerperal period and defined by ICD-10 (code O85) as a complication of the puerperium with endometritis, fever, peritonitis and septicemia, but excluding obstetric pyemic and septic embolism, and septicaemia during labour. Puerperal infection is a more general term than puerperal sepsis to indicate any infection after delivery. Although pathogens of puerperal infections are known to be mostly aerobic bacteria (approx. 80%) derived from maternal vaginal flora, maternal intestinal flora, and environment, little is known about their species and frequencies, and genetic characteristics. In the present study, I analyzed aerobic bacteria isolated from puerperal infections for two years in Bangladesh on spectrum and prevalence of bacterial species, and their susceptibility to various antimicrobials. In particular, prevalence of important resistance genes and virulence factors, and phylogenetic traits were investigated for *S. aureus* and *E. coli*, the important causes of puerperal infections.

Clinical isolates of aerobic bacteria were isolated from patients with puerperal infections who visited Mymensingh Medical College hospital, in Mymensingh, Bangladesh (2011-2012). MIC against various antimicrobials was measured for each isolate by broth microdilution test using Dry Plate Eiken DP32 and DP31. Extended-spectrum beta-lactamase (ESBL) was screened by double-disk synergy test. Detection and characterization of beta-lactamase were performed by multiplex PCR, and PCR and direct sequencing. For *S. aureus*, coagulase genotype, ST, and SCC mec type were determined, and resistance genes and virulence factors were detected by PCR. For *E. coli*, phylogenetic group, ST (Achtman’s scheme) were determined and PCR was used to detect O25b allele, *aac(6')-Ib-cr*, and virulence factors.

During the 2-year study period, from a total of 676 specimens, 470 isolates of aerobic bacteria (209 Gram-positive cocci and 261 Gram-negative rods isolates) were obtained. The most common species was *E. coli* (n=98), followed by *E. faecalis* (n=54), *S. haemolyticus* (n=33), *P. mirabilis* (n=32), *S. aureus* (n=27), *K. pneumoniae* (n=22), and *E. cloacae* (n=21). Among Gram-positive cocci, *S. aureus* was isolated at significantly higher rate from wound (19.8%, 17/86) than endocervical swab (7.6%, 6/79) or urine (9.1%, 4/44). Similarly, *A. baumanii* and *B. cepacia* were
detected mostly in wound swabs. In contrast, *E. coli* were isolated from endometritis and urinary tract infections (endocervical swab and urine) at significantly higher proportion (54% and 50%, respectively) than wound infections (10%). All the Gram-positive cocci tested were susceptible to VCM, TEC, LZD, and FOI. Gram-negative rods exhibited high resistance rates to cephalosporins (e.g., third-generation cephalosporins: CTX, 78-96%; CAZ, 61-91%). *A. baumanii* showed higher rates of resistance to IPM and MEM (44% and 50%, respectively) than enterobacteriaceae (<9% and <18%, respectively). *E. coli* showed higher resistance rates to LVX and SXT than aminoglycosides and MIN. Except for *A. baumanii*, all the Gram-negative rod species were nearly susceptible to FOI, while *A. baumanii* isolates were mostly susceptible to LVX and SXT.

Most of *E. coli* isolates were resistant to cephalosporins harboring *bla*CTX-M group 1. Phylogroup B2 isolates with *bla*CTX-M-15 were classified into ST131 with O25b allele, harboring aac(6’)-Ib-cr and various virulence factors. *E. coli* with these characteristics have been recognized as international pandemic clone with increased drug resistance and virulence, frequently causing community-onset and extraintestinal infections. Carbapenemase genes *bla*NDM-1 and *bla*NDM-7 were identified in one isolate each of phylogroup A *E. coli* belonging to ST90 and ST167, respectively. Pandemic clone of *E. coli* (B2-ST131) and an *E. coli* with *bla*NDM-7 from humans were detected for the first time in Bangladesh in the present study.

Methicillin-resistant *S. aureus* (MRSA) had type IV or V SCCmec, containing isolates classified into ST361 (CC672), which is related to an emerging clone ST672 in Indian subcontinent. PVL gene was detected in one-third of *S. aureus* isolates, although only one PVL-positive isolate was MRSA belonging to ST6. Among the PVL-positive *S. aureus*, ST772 which had been referred to as “Bengal Bay clone” was identified.

In this study, species, frequencies, and drug resistance of aerobic bacteria causing puerperal infections in Bangladesh were elucidated, and genetic traits of *S. aureus* and *E. coli* were further characterized. The obtained information will be useful for reexamining the use of antimicrobial agents to improve clinical practice for puerperal infections and control drug-resistant bacteria. Furthermore, the present study indicated the need for further analysis of common species other than *E. coli* and *S. aureus*, including coagulase-negative staphylococci and *E. faecalis*, and also for continuous surveillance of some important drug-resistant clones represented by ST131 *E. coli*.